

# *Meis3* Cas9-KO Strategy

**Designer:**

**Huimin Su**

**Reviewer:**

**Ruirui Zhang**

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# Project Overview

**Project Name**

*Meis3*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Meis3* gene. The schematic diagram is as follows:



- The *Meis3* gene has 9 transcripts. According to the structure of *Meis3* gene, exon2-exon11 of *Meis3-201* (ENSMUST00000002495.17) transcript is recommended as the knockout region. The region contains 1075bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Meis3* gene. The brief process is as follows: CRISPR/Cas9 system w

- The *Meis3* gene is located on the Chr7. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



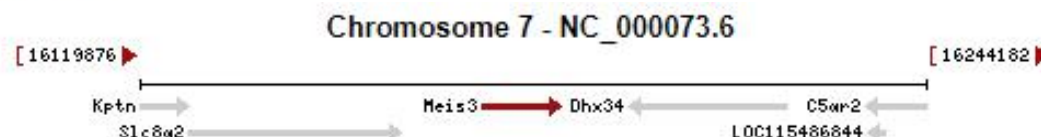
# Gene information (NCBI)

## Meis3 Meis homeobox 3 [ *Mus musculus* (house mouse) ]

Gene ID: 17537, updated on 20-Aug-2019

### Summary

Official Symbol	Meis3 provided by <a href="#">MGI</a>
Official Full Name	Meis homeobox 3 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:108519</a>
See related	<a href="#">Ensembl:ENSMUSG00000041420</a>
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mrg2; AI573393
Summary	The protein encoding this gene belongs to the three amino acid loop extension family of homeodomain transcription factors, which play essential roles in many embryonic processes. These proteins are characterized by an atypical homeodomain containing a three amino acid loop extension between helices 1 and 2. Expression of this gene begins during the compaction stage of embryogenesis and continues into the blastocyst stage. This gene is also expressed in pancreatic islet cells and beta-cells and regulates beta-cell survival. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Nov 2014]
Expression	Broad expression in whole brain E14.5 (RPKM 38.1), CNS E14 (RPKM 35.8) and 21 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

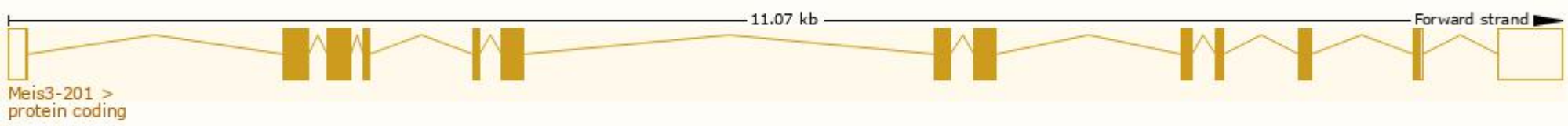


# Transcript information (Ensembl)

The gene has 9 transcripts,all transcripts are shown below:

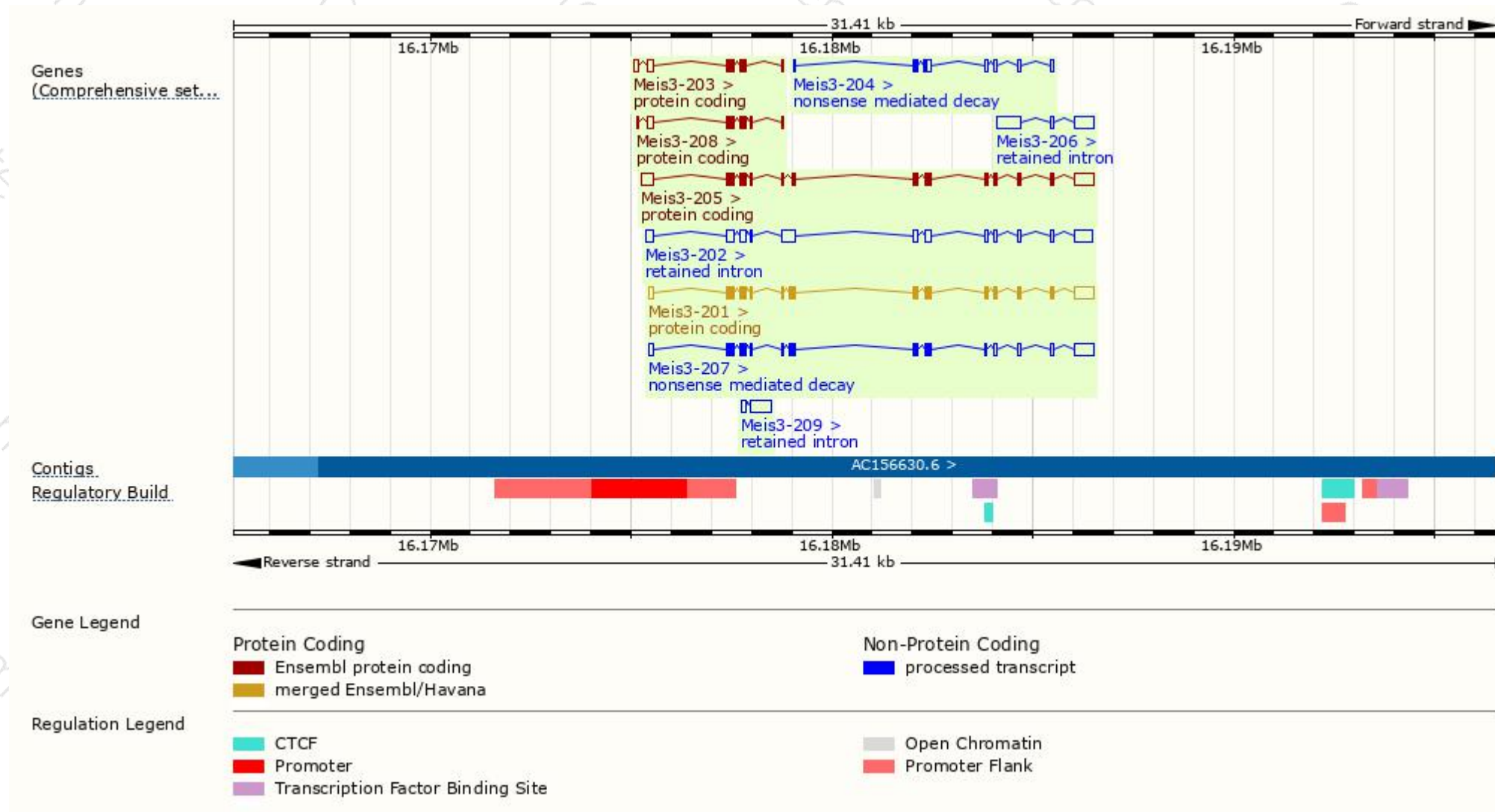
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Meis3-205	<a href="#">ENSMUST00000176506.7</a>	1839	<a href="#">361aa</a>	Protein coding	<a href="#">CCDS71892</a>	<a href="#">P97368</a>	TSL:1 GENCODE basic
Meis3-201	<a href="#">ENSMUST00000002495.17</a>	1731	<a href="#">378aa</a>	Protein coding	<a href="#">CCDS39782</a>	<a href="#">P97368</a>	TSL:1 GENCODE basic APPRIS P1
Meis3-203	<a href="#">ENSMUST00000176342.7</a>	659	<a href="#">134aa</a>	Protein coding	-	<a href="#">H3BK94</a>	CDS 3' incomplete TSL:3
Meis3-208	<a href="#">ENSMUST00000177540.7</a>	659	<a href="#">150aa</a>	Protein coding	-	<a href="#">H3BKH0</a>	CDS 3' incomplete TSL:3
Meis3-207	<a href="#">ENSMUST00000177156.7</a>	1724	<a href="#">313aa</a>	Nonsense mediated decay	-	<a href="#">Q148B2</a>	TSL:1
Meis3-204	<a href="#">ENSMUST00000176446.1</a>	640	<a href="#">84aa</a>	Nonsense mediated decay	-	<a href="#">H3BJ55</a>	CDS 5' incomplete TSL:5
Meis3-202	<a href="#">ENSMUST00000175946.7</a>	1925	No protein	Retained intron	-	-	TSL:2
Meis3-206	<a href="#">ENSMUST00000176714.2</a>	1147	No protein	Retained intron	-	-	TSL:2
Meis3-209	<a href="#">ENSMUST00000183527.1</a>	637	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Meis3-201* transcript,The transcription is shown below





# Genomic location distribution





# Protein domain



If you have any questions, you are welcome to inquire.

Tel: 400-9660890

